



SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> A novel polypeptide, a cDNA encoding the polypeptide and utilization thereof

<130> Q61531

<140> 09/674,379

<141> 2000-10-30

<150> PCT/JP99/02284

<151> 1999-04-28

<150> JP 10-119731

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<170> PatentIn version 3.1

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Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile
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Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
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Arg	Gly	Asp	Met	Met	Cys	Val	Asn	Gln	Asn	Gly	Gly	Tyr	Leu	Cys	Ile		
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Pro	Arg	Thr	Asn	Pro	Val	Tyr	Arg	Gly	Pro	Tyr	Ser	Asn	Pro	Tyr	Ser		
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Thr	Ser	Tyr	Ser	Gly	Pro	Tyr	Pro	Ala	Ala	Ala	Pro	Pro	Val	Pro	Ala		
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Ser	Asn	Tyr	Pro	Thr	Ile	Ser	Arg	Pro	Leu	Val	Cys	Arg	Phe	Gly	Tyr		
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Gln	Met	Asp	Glu	Gly	Asn	Gln	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	Thr		
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Asp	Ser	His	Gln	Cys	Asn	Pro	Thr	Gln	Ile	Cys	Ile	Asn	Thr	Glu	Gly		
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Gly	Tyr	Thr	Cys	Ser	Cys	Thr	Asp	Gly	Tyr	Trp	Leu	Leu	Glu	Gly	Gln		
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Cys	Leu	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Gly	Tyr	Cys	Gln	Gln	Leu	Cys		
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Leu	Asn	Asp	Asp	Gly	Arg	Ser	Cys	Gln	Asp	Val	Asn	Glu	Cys	Glu	Thr		
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gag	aat	ccc	tgt	gtt	cag	acc	tgt	gtc	aac	acc	tat	ggc	tct	ttc	atc		957
Glu	Asn	Pro	Cys	Val	Gln	Thr	Cys	Val	Asn	Thr	Tyr	Gly	Ser	Phe	Ile		
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Cys	Arg	Cys	Asp	Pro	Gly	Tyr	Glu	Leu	Glu	Glu	Asp	Gly	Ile	His	Cys		
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Ser	Asp	Met	Asp	Glu	Cys	Ser	Phe	Ser	Glu	Phe	Leu	Cys	Gln	His	Glu	
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Cys	Val	Asn	Gln	Pro	Gly	Ser	Tyr	Phe	Cys	Ser	Cys	Pro	Pro	Gly	Tyr	
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gtc	ctg	ttg	gat	gat	aac	cga	agc	tgc	cag	gat	atc	aat	gaa	tgt	gag	1149
Val	Leu	Leu	Asp	Asp	Asn	Arg	Ser	Cys	Gln	Asp	Ile	Asn	Glu	Cys	Glu	
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His	Arg	Asn	His	Thr	Cys	Thr	Ser	Leu	Gln	Thr	Cys	Tyr	Asn	Leu	Gln	
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Gly	Gly	Phe	Lys	Cys	Ile	Asp	Pro	Ile	Ser	Cys	Glu	Glu	Pro	Tyr	Leu	
			290					295					300			
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Leu	Ile	Gly	Glu	Asn	Arg	Cys	Met	Cys	Pro	Ala	Glu	His	Thr	Ser	Cys	
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Arg	Asp	Gln	Pro	Phe	Thr	Ile	Leu	Tyr	Arg	Asp	Met	Asp	Val	Val	Ser	
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Tyr	Pro	Gly	Ala	Tyr	Tyr	Ile	Phe	Gln	Ile	Lys	Ser	Gly	Asn	Glu	Gly	
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cga	gag	ttc	tat	atg	cgg	caa	aca	ggg	cct	atc	agt	gcc	acc	ctg	gtg	1485
Arg	Glu	Phe	Tyr	Met	Arg	Gln	Thr	Gly	Pro	Ile	Ser	Ala	Thr	Leu	Val	
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atg	aca	cgc	ccc	atc	aaa	ggg	cct	cgg	gac	atc	cag	ctg	gac	ttg	gag	1533
Met	Thr	Arg	Pro	Ile	Lys	Gly	Pro	Arg	Asp	Ile	Gln	Leu	Asp	Leu	Glu	
		385					390					395				
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Met	Ile	Thr	Val	Asn	Thr	Val	Ile	Asn	Phe	Arg	Gly	Ser	Ser	Val	Ile	
	400					405					410					
cga	ctg	cgg	ata	tat	gtg	tcg	cag	tat	ccg	ttc	tgagcctctg	gctaaggcct				1634
Arg	Leu	Arg	Ile	Tyr	Val	Ser	Gln	Tyr	Pro	Phe						
415					420				425							
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gagcgagaca	gacattgcac	ctttcctgct	gaatatctcc	tgggggcatc	agcctagcat											1754

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<210> 8
 <211> 461
 <212> PRT
 <213> Mus musculus

<220>
 <221> misc_feature
 <223> Clone mouse A55b derived from Day 13 mouse embryonic heart

<400> 8

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Arg Arg Met Ile Leu Thr Val Thr Ile Leu Ala Leu Trp Leu Pro His
 -20 -15 -10 -5

Pro Gly Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg
 -1 1 5 10

Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu
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Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu
 30 35 40

Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro
 45 50 55 60

Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val
 65 70 75

Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe
 80 85 90

Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys
 95 100 105

Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr
 110 115 120

Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu
 125 130 135 140

Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln
 145 150 155

Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly
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Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys
 175 180 185

Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser
 190 195 200

Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile
 205 210 215 220

His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln
 225 230 235

His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro
 240 245 250

Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu

255

260

265

Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn
 270 275 280

Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro
 285 290 295 300

Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr
 305 310 315

Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val
 320 325 330

Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr
 335 340 345

Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn
 350 355 360

Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr
 365 370 375 380

Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp
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<211> 423

<212> PRT

<213> Mus musculus

<400> 9

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Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
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Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser
 50 55 60

Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro
 65 70 75 80

Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu
 85 90 95

Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
 100 105 110

Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
 115 120 125

Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
 130 135 140

Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro
 145 150 155 160

Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp
 165 170 175

Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys
 180 185 190

Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
 195 200 205

Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp
 210 215 220

Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
 225 230 235 240

Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp
245 250 255

Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
260 265 270

Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys
275 280 285

Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu
290 295 300

Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro
305 310 315 320

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
325 330 335

Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
340 345 350

Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
355 360 365

Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
370 375 380

Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val
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Tyr Val Ser Gln Tyr Pro Phe
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<211> 1269
<212> DNA
<213> Mus musculus

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acatcctact caggcccata cccagcagcg gccccaccag taccagcttc caactacccc	240
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gtggatgtgg acgagtgtgc aacagactca caccagtgc accctacca gatctgtatc	360
aacactgaag gaggttacac ctgctcctgc accgatgggt actggcttct ggaagggcag	420
tgccatagata ttgatgaatg tcgctatggt tactgccagc agctctgtgc aaatgttcca	480
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 <212> DNA
 <213> Homo sapiens

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ttagatattg atgaatgccg aaccatcccc gaggcctgcc gaggagacat gatgtgtgtt	180

aaccaaaatg gcggggtat	atgcattccc	cggacaaacc	ctgtgtatcg	agggccctac	240
tcgaaacctt actcgacccc	ctactcaggt	ccgtaccag	cagctgcccc	accactctca	300
gctccaaact atcccacgat	ctccaggcct	cttatatgcc	gctttggata	ccagatggat	360
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gatggcgttc attgcagtga	tatggacgag	tgagcttct	ctgagttcct	ctgccaacat	780
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agtgccaccc tggatgatgac	acgccccatc	aaagggcccc	gggaaatcca	gctggacttg	1260
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<210> 12
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Clone human A55 derived from human brain

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 <221> CDS
 <222> (169)..(1512)

<223>

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<221> sig_peptide

<222> (169)..(237)

<223>

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<222> (238)..(1512)

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cgcgagcttt cttctcgct tcgcatctcc tcctcgcgcg tcttggac atg cca gga 177
Met Pro Gly

ata aaa agg ata ctc act gtt acc att ctg gct ctc tgt ctt cca agc 225
Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys Leu Pro Ser
-20 -15 -10 -5

cct ggg aat gca cag gca cag tgc acg aat ggc ttt gac ctg gat cgc 273
Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg
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cag tca gga cag tgt tta gat att gat gaa tgc cga acc atc ccc gag 321
Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu
15 20 25

gcc tgc cga gga gac atg atg tgt gtt aac caa aat ggc ggg tat tta 369
Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu
30 35 40

tgc att ccc cgg aca aac cct gtg tat cga ggg ccc tac tcg aac ccc 417
Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro
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Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu
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Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe
80 85 90

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Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val Asp Glu Cys
95 100 105

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Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr	
110 115 120	
gaa ggc ggg tac acc tgc tcc tgc acc gac gga tat tgg ctt ctg gaa	657
Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu	
125 130 135 140	
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Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln	
145 150 155	
ctc tgt gcg aat gtt cct gga tcc tat tct tgt aca tgc aac cct ggt	753
Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly	
160 165 170	
ttt acc ctc aat gag gat gga agg tct tgc caa gat gtg aac gag tgt	801
Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys	
175 180 185	
gcc acc gag aac ccc tgc gtg caa acc tgc gtc aac acc tac ggc tct	849
Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser	
190 195 200	
ttc atc tgc cgc tgt gac cca gga tat gaa ctt gag gaa gat ggc gtt	897
Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val	
205 210 215 220	
cat tgc agt gat atg gac gag tgc agc ttc tct gag ttc ctc tgc caa	945
His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln	
225 230 235	
cat gag tgt gtg aac cag ccc ggc aca tac ttc tgc tcc tgc cct cca	993
His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro	
240 245 250	
ggc tac atc ctg ctg gat gac aac cga agc tgc caa gac atc aac gaa	1041
Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu	
255 260 265	
tgt gag cac agg aac cac acg tgc aac ctg cag cag acg tgc tac aat	1089
Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn	
270 275 280	
tta caa ggg ggc ttc aaa tgc atc gac ccc atc cgc tgt gag gag cct	1137
Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro	
285 290 295 300	
tat ctg agg atc agt gat aac cgc tgt atg tgt cct gct gag aac cct	1185
Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala Glu Asn Pro	
305 310 315	
ggc tgc aga gac cag ccc ttt acc atc ttg tac cgg gac atg gac gtg	1233
Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val	

320	325	330	
gtg tca gga cgc tcc gtt ccc gct gac atc ttc caa atg caa gcc acg			1281
Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr			
335	340	345	
acc cgc tac cct ggg gcc tat tac att ttc cag atc aaa tct ggg aat			1329
Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn			
350	355	360	
gag ggc aga gaa ttt tac atg cgg caa acg ggc ccc atc agt gcc acc			1377
Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr			
365	370	375	380
ctg gtg atg aca cgc ccc atc aaa ggg ccc cgg gaa atc cag ctg gac			1425
Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp			
385	390	395	
ttg gaa atg atc act gtc aac act gtc atc aac ttc aga ggc agc tcc			1473
Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser			
400	405	410	
gtg atc cga ctg cgg ata tat gtg tcg cag tac cca ttc tgagcctcgg			1522
Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe			
415	420	425	
gctggagcct ccgacgctgc ctctcattgg caccaaggga caggagaaga gaggaaataa			1582
cagagagaat gagagcgaca cagacgttag gcatttcctg ctgaacgttt ccccgaagag			1642
tcagccccga cttcctgact ctcacctgta ctattgcaga cctgtcacc tgcaggactt			1702
gccacccccca gttcctatga tacagttatc aaaaagtatt atcattgctc ccctgataga			1762
agattgttgg tgaattttca aggcccttcag tttattttcca ctattttcaa agaaaataga			1822
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gggaaccctg ggagtagcta gtttgctttt tgcgtacaca gagaaggcta tgtaaacaaa			2002
ccacagcagg atcgaagggt ttttagagaa tgtgtttcaa aaccatgcct ggtattttca			2062
accataaaaag aagtttcagt tgtccttaaa tttgtataac ggtttaattc tgtcttgttc			2122
attttgagta tttttaaaaa atatgtcgta gaattccttc gaaaggcctt cagacacatg			2182
ctatgttctg tcttcccaa cccagtctcc tctccatttt agcccagtgt tttctttgag			2242
gaccccttaa tcttgctttc tttagaattt ttacccaatt ggattggaat gcagaggtct			2302
ccaaactgat taaatatttg aagaga			2328

<210> 13
<211> 448
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Clone human A55 derived from human brain

<400> 13

Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys
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Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp
-5 -1 1 5

Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
10 15 20 25

Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
30 35 40

Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
45 50 55

Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
60 65 70

Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
75 80 85

Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
90 95 100 105

Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
110 115 120

Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
125 130 135

Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
140 145 150

Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
 155 160 165

Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
 170 175 180 185

Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
 190 195 200

Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
 205 210 215

Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
 220 225 230

Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
 235 240 245

Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
 250 255 260 265

Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
 270 275 280

Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
 285 290 295

Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
 300 305 310

Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
 315 320 325

Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
 330 335 340 345

Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
 350 355 360

Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
 365 370 375

Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile
380 385 390

Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
395 400 405

Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
410 415 420 425

<210> 14
<211> 423
<212> PRT
<213> Homo sapiens

<400> 14

Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu
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Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met
20 25 30

Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
35 40 45

Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro Tyr Ser
50 55 60

Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn Tyr Pro
65 70 75 80

Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met Asp Glu
85 90 95

Ser Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
100 105 110

Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
115 120 125

Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
130 135 140

Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro
145 150 155 160

Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Glu Asp
165 170 175

Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Ala Thr Glu Asn Pro Cys
180 185 190

Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
195 200 205

Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val His Cys Ser Asp Met Asp
210 215 220

Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
225 230 235 240

Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Ile Leu Leu Asp
245 250 255

Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
260 265 270

Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys
275 280 285

Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser Asp
290 295 300

Asn Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp Gln Pro
305 310 315 320

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
325 330 335

Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
340 345 350

Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
355 360 365

Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
 370 375 380

Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu Glu Met Ile Thr Val
 385 390 395 400

Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile
 405 410 415

Tyr Val Ser Gln Tyr Pro Phe
 420

<210> 15
 <211> 1269
 <212> DNA
 <213> Homo sapiens

<400> 15
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 tattttatgca ttccccggac aaaccctgtg tatcgagggc cctactcgaa cccctactcg 180
 accccctact caggctcgta cccagcagct gccccaccac tctcagctcc aaactatccc 240
 acgatctcca ggctctttat atgccgcttt ggataccaga tggatgaaag caaccaatgt 300
 gtggatgtgg acgagtgtgc aacagattcc caccagtgc accccacca gatctgcatc 360
 aatactgaag gcgggtacac ctgctcctgc accgacggat attggcttct ggaaggccag 420
 tgcttagaca ttgatgaatg tcgctatggt tactgccagc agctctgtgc gaatgttcct 480
 ggatcctatt cttgtacatg caaccctggg tttaccctca atgaggatgg aaggctctgc 540
 caagatgtga acgagtgtgc caccgagaac cctgcgtgc aaacctgcgt caacacctac 600
 ggctctttca tctgccgctg tgaccagga tatgaacttg aggaagatgg cgttcattgc 660
 agtgatatgg acgagtgcag cttctctgag ttctctgcc aacatgagtg tgtgaaccag 720
 cccggcacat acttctgctc ctgccctcca ggctacatcc tgctggatga caaccgaagc 780
 tgccaagaca tcaacgaatg tgagcacagg aaccacacgt gcaacctgca gcagacgtgc 840
 tacaatttac aaggggggctt caaatgcatc gaccccatcc gctgtgagga gccttatctg 900
 aggatcagtg ataaccgctg tatgtgtcct gctgagaacc ctggctgcag agaccagccc 960

tttaccatct tgtaccggga catggacgtg gtgtcaggac gtcctgttcc cgctgacatc 1020
 ttccaaatgc aagccacgac ccgctaccct ggggcctatt acattttcca gatcaaactc 1080
 ggggaatgagg gcagagaatt ttacatgcgg caaacggggc ccatcagtgc caccctggtg 1140
 atgacacgcc ccatcaaagg gccccgggaa atccagctgg acttggaat gatcactgtc 1200
 aacactgtca tcaacttcag aggcagctcc gtgatccgac tgcggatata tgtgtcgcag 1260
 taccattc 1269

<210> 16
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> misc_feature
 <222> (27)..(35)
 <223> "n" may be a, c, g or t

<400> 16 35
 cgattgaatt ctagacctgc ctcgagnnnn nnnnn

<210> 17
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 17 27
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